



1600

RAW SEQUENCE LISTING

DATE: 08/01/2003

PATENT APPLICATION: US/09/973,382B

TIME: 14:40:52

Input Set : N:\Crf4\07302003\I973282B.raw

Output Set: N:\CRF4\08012003\I973382B.raw

1 <110> APPLICANT: Heston, Warren D.W.
 2 O'Keefe, Denise S.
 3 <120> TITLE OF INVENTION: DNA Encoding the Prostate-Specific Membrane
 4 Antigen-Like Gene and Uses Thereof
 5 <130> FILE REFERENCE: D6230
 C--> 6 <140> CURRENT APPLICATION NUMBER: US/09/973,382B
 7 <141> CURRENT FILING DATE: 2001-10-09
 8 <150> PRIOR APPLICATION NUMBER: PCT/US00/09417
 9 <151> PRIOR FILING DATE: 2000-04-09
 10 <160> NUMBER OF SEQ ID NOS: 38
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 1992
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Homo sapiens
 16 <220> FEATURE:
 17 <223> OTHER INFORMATION: cDNA sequence of PSMA-like gene
 18 <400> SEQUENCE: 1
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 21 gatgtccttt tttgttaggcc taatgacaaa aggttgaaga taaagttcta 150
 22 gtactcattt aagtgtataa ttgaaaattt atattacca atctggaaaca 200
 23 accaatttaa aataaggaaa gaaagacact gtgtttctta gttaaaaat 250
 24 gcccagctgg caggggccaa aggagtctt ctctactcag accctgctga 300
 25 ctactttgtt cctgggtgtt agtccatatcc agacgggtgg aatcttccctg 350
 26 gaggtgggtt ccagcgttgg aatatcctaa atctgaatgg tgcaaggagac 400
 27 cctctcacac caggttaccc agcaaatgaa tacgcttata ggcatggaat 450
 28 tgcagaggct gttggcttca caagtattcc tggcatcca gttggataact 500
 29 atgatgcaca gaagctccta gaaaaatgg gtggctcagc accaccagat 550
 30 agcagcttgg aggaaagtct caaatgttcc tacaatgtt gacctggctt 600
 31 tactggaaac ttttctacac aaaaagtcaa gatgcacatc cactctacca 650
 32 atgaagtgc gagaattttac aatgtgtatag gtactctcag aggagcagt 700
 33 gaaccagaca gatatgtcat tctggaggt caccggact catgggtgtt 750
 34 tgggtgtatt gaccctcaga gtggagcagc tggatgttcat gaaactgtga 800
 35 ggagctttgg aacactgaaa aaggaagggt ggagacctag aagaacaatt 850
 36 ttgtttgcaa gctggatgc agaagaattt ggtcttctt gttctactga 900
 37 gtgggcagag gataattcaa gactccttca agagcgtggc gtggcttata 950
 38 ttaatgctga ctcatctata gaaggaaact acactctgag agttgattgt 1000
 39 acaccactga tgcacatgtt ggtataacaac ctaacaaaag agctaaaaag 1050
 40 ccctgtatgaa ggcttggaa gcaaatctt ttatgaaatg tggactaaaa 1100
 41 aaagtcccttc cccagagttc agtggcatgc ccaggataag caaattggga 1150
 42 tctggaaatg attttgaggt gttcttccaa cgacttggaa ttgcttcagg 1200
 43 cagagcacgg tataactaaaa attggaaac aaacaaattc agcggctatc 1250
 44 cactgtatca cagtgtctat gaaacatatg agttgggtggaa aagttttat 1300

Does Not Comply
 Corrected Diskette Needed

7.3

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45 gatccaatgt ttaaatatca cctcaactgtg gcccaggttc gaggagggat 1350
 46 ggtgtttgag ctagccaatt ccatagtgct ccctttgtat tgcgagatt 1400
 47 atgctgttagt tttaagaaaag tatgctgaca aaatctacaa tatttctatg 1450
 48 aaacatccac agggaaatgaa gacatacagt ttatcatttgc attcacttt 1500
 49 ttctgcagta aaaaatttta cagaaattgc ttccaagttc agcgagagac 1550
 50 tccaggactt tgacaaaagc aacccaatat tggtaagaat gatgaatgt 1600
 51 caactcatgt ttctggaaag agoatttatt gatccattag gtttaccaga 1650
 52 cagacctttt tataaggcatg tcatactatgc tccaaggcgc cacaacaagt 1700
 53 atgcagggga gtcattccca ggaattttagt atgctctgtt tgatattgaa 1750
 54 agcaaagtgg acccttccaa ggcctgggg gatgtgaaga gacagatttc 1800
 55 tggcagcc ttcacagtgc aggcaactgc agagactttg agtgaagtag 1850
 56 ccttaagagga ttcttttagag actctgtatt gaatttgggtt ggtatgtcac 1900
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 61 <211> LENGTH: 442
 62 <212> TYPE: PRT
 63 <213> ORGANISM: Homo sapiens
 64 <220> FEATURE:
 65 <223> OTHER INFORMATION: deduced amino acid sequence of PSMA-like
 66 protein
 67 <400> SEQUENCE: 2
 68 Met Gly Gly Ser Ala Pro Pro Asp Ser Ser Trp Arg Gly Ser Leu
 69 5 10 15
 70 Lys Val Ser Tyr Asn Val Gly Pro Gly Phe Thr Gly Asn Phe Ser
 71 20 25 30
 72 Thr Gln Lys Val Lys Met His Ile His Ser Thr Asn Glu Val Thr
 73 35 40 45
 74 Arg Ile Tyr Asn Val Ile Gly Thr Leu Arg Gly Ala Val Glu Pro
 75 50 55 60
 76 Asp Arg Tyr Val Ile Leu Gly Gly His Arg Asp Ser Trp Val Phe
 77 65 70 75
 78 Gly Gly Ile Asp Pro Gln Ser Gly Ala Ala Val Val His Glu Thr
 79 80 85 90
 80 Val Arg Ser Phe Gly Thr Leu Lys Lys Glu Gly Trp Arg Pro Arg
 81 95 100 105
 82 Arg Thr Ile Leu Phe Ala Ser Trp Asp Ala Glu Glu Phe Gly Leu
 83 110 115 120
 84 Leu Gly Ser Thr Glu Trp Ala Glu Asp Asn Ser Arg Leu Leu Gln
 85 125 130 135
 86 Glu Arg Gly Val Ala Tyr Ile Asn Ala Asp Ser Ser Ile Glu Gly
 87 140 145 150
 88 Asn Tyr Thr Leu Arg Val Asp Cys Thr Pro Leu Met Tyr Ser Leu
 89 155 160 165
 90 Val Tyr Asn Leu Thr Lys Glu Leu Lys Ser Pro Asp Glu Gly Phe
 91 170 175 180
 92 Glu Gly Lys Ser Leu Tyr Glu Ser Trp Thr Lys Lys Ser Pro Ser
 93 185 190 195
 94 Pro Glu Phe Ser Gly Met Pro Arg Ile Ser Lys Leu Gly Ser Gly

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95 200 205 210
 96 Asn Asp Phe Glu Val Phe Phe Gln Arg Leu Gly Ile Ala Ser Gly
 97 215 220 225
 98 Arg Ala Arg Tyr Thr Lys Asn Trp Glu Thr Asn Lys Phe Ser Gly
 99 230 235 240
 100 Tyr Pro Leu Tyr His Ser Val Tyr Glu Thr Tyr Glu Leu Val Glu
 101 245 250 255
 102 Lys Phe Tyr Asp Pro Met Phe Lys Tyr His Leu Thr Val Ala Gln
 103 260 265 270
 104 Val Arg Gly Gly Met Val Phe Glu Leu Ala Asn Ser Ile Val Leu
 105 275 280 285
 106 Pro Phe Asp Cys Arg Asp Tyr Ala Val Val Leu Arg Lys Tyr Ala
 107 290 295 300
 108 Asp Lys Ile Tyr Asn Ile Ser Met Lys His Pro Gln Glu Met Lys
 109 305 310 315
 110 Thr Tyr Ser Leu Ser Phe Asp Ser Leu Phe Ser Ala Val Lys Asn
 111 320 325 330
 112 Phe Thr Glu Ile Ala Ser Lys Phe Ser Glu Arg Leu Gln Asp Phe
 113 335 340 345
 114 Asp Lys Ser Asn Pro Ile Leu Leu Arg Met Met Asn Asp Gln Leu
 115 350 355 360
 116 Met Phe Leu Glu Arg Ala Phe Ile Asp Pro Leu Gly Leu Pro Asp
 117 365 370 375
 118 Arg Pro Phe Tyr Arg His Val Ile Tyr Ala Pro Ser Ser His Asn
 119 380 385 390
 120 Lys Tyr Ala Gly Glu Ser Phe Pro Gly Ile Tyr Asp Ala Leu Phe
 121 395 400 405
 122 Asp Ile Glu Ser Lys Val Asp Pro Ser Lys Ala Trp Gly Asp Val
 123 410 415 420
 124 Lys Arg Gln Ile Ser Val Ala Ala Phe Thr Val Gln Ala Ala Ala
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129 <210> SEQ ID NO: 3
 130 <211> LENGTH: 2653
 131 <212> TYPE: DNA

132 <213> ORGANISM: Homo sapiens
 133 <220> FEATURE:
 134 <223> OTHER INFORMATION: nucleotide sequence of human PSMA gene

135 <300> PUBLICATION INFORMATION:

136 <308> DATABASE ACCESSION NO: GenBank Accession No. M99487

W--> 137 <309> DATABASE ENTRY DATE: *mandatory response needed whenever <308> has a response.*
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 139 ctcaaaaggg gccggatttc ctctcctgg aggcatgtgt tgcctctc 50
 140 tctcgctcggtt atgggttcag tgcactctag aaacactgct gtgggtggaga 100
 141 aactggaccc caggtctgga gccaattcca gcctgcagggtt ctgataagcg 150
 142 aggcatgtt gagattgaga gagactttac cccgcctgg tggttggagg 200
 143 gcgcgacta gaggcagc acaggcgcgg gtccccggag gcccggctctg 250
 144 ctcgcgccga gatgtgaaat ctcccttcacg aaaccgactc ggctgtggcc 300

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145 accgcgcgcc gcccgcgtg gctgtgcgt ggggcgtgg tgctggcggg 350
 146 tggcttcttt ctccctcggt tcctcttcgg gtggtttata aaatcctcca 400
 147 atgaagctac taacattact ccaaaggata atatgaaagc atttttggat 450
 148 gaattgaaag ctgagaacat caagaagttc ttatataatt ttacacagat 500
 149 accacattta gcaggaacag aacaaaactt tcagcttgc aagcaaattc 550
 150 aatcccagtg gaaagaattt ggcctggatt ctgttggact agcacattat 600
 151 gatgtcctgt tgccttaccc aaataagact catcccaact acatctcaat 650
 152 aattaatgaa gatggaaatg agatttcaaa cacatcatta tttgaaccac 700
 153 ctccctccagg atatgaaaat gtttggata ttgtaccacc tttcagtgt 750
 154 ttctctcctc aaggaatgcc agagggcgat ctatgtatg ttaactatgc 800
 155 acgaactgaa gacttctta aatttggaaacg ggacatgaaa atcaattgct 850
 156 ctggaaaaat tgcatttgc agatatggg aagtttcag agggaaataag 900
 157 gttaaaaatg cccagctggc aggggccaaa ggagtccattc tctactccga 950
 158 ccctgctgac tactttgtc ctgggggtgaa gtcctatcca gatgggttgg 1000
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 161 gcgtggatt gcagggctg ttgggtttcc aagtattcc tttcatccaa 1150
 162 ttggatacta tgcatttgc aagcttcttag aaaaaatggg tggctcagca 1200
 163 ccaccagata gcagctggag agaagtctc aaagtgcctt acaatgttgg 1250
 164 acctggctt actggaaact tttctacaca aaaagtcaag atgcacatcc 1300
 165 actctaccaa tgaagtgaca agaatttaca atgtgatagg tactctcaga 1350
 166 ggagcagtgg aaccagacag atatgtcatt ctgggggtc accgggactc 1400
 167 atgggtgttt ggtggattt accctcagag tggagcagct gttgttcatg 1450
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 176 tgcttcaggc agagcacggt atactaaaaaa ttggggaaaca aacaaattca 1900
 177 gcccgtatcc actgtatcac agtgcgtatg aaacatatgaa gttgggtggaa 1950
 178 aagttttatg atccaatgtt taaatatcac ctcactgtgg cccaggttcg 2000
 179 aggagggatg gtgtttggc tagccaaatc catatgtctc ccttttgatt 2050
 180 gtcgagatgtt tgctgtatgtt ttaagaaaatg atgctgacaa aatctacagt 2100
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 182 ttcaactttt tctgcagtaa agaattttac agaatttgc tccaaatgttca 2200
 183 gtgagagact ccaggactttt gacaaaaggca acccaatagt attaagaatg 2250
 184 atgaatgtc aactcatgtt tctggaaatgaaatg gcatttatttgc atccatttgg 2300
 185 gttaccagac aggcctttt ataggcatgtt catctatgtt ccaaggagcc 2350
 186 acaacaagta tgcaggggag tcattcccgat gaatttgc tgcgtgttt 2400
 187 gatattgaaa gcaaagtggc cccttccaaatg gcctggggag aagtgaagag 2450
 188 acagattttat gttgcagccat tcacagtgc ggcagctgc gagaacttgc 2500
 189 gtgaagttagc ctaagaggat tcttttagaga atccgtatttgc aatttgcgtt 2550
 190 gtatgtcaatc cagaaagaat cgtaaatgggtt atattgataa attttaaaat 2600
 191 tggtatattt gaaataaagt tgaatattat atataaaaaaaa aaaaaaaaaaa 2650
 192 aaa 2653
 194 <210> SEQ ID NO: 4

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Input Set : N:\Crf4\07302003\I973282B.raw

Output Set: N:\CRF4\08012003\I973382B.raw

195 <211> LENGTH: 750
 196 <212> TYPE: PRT
 197 <213> ORGANISM: Homo sapiens
 198 <220> FEATURE:
 199 <223> OTHER INFORMATION: deduced amino acid sequence of PSMA protein
 200 <400> SEQUENCE: 4

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204					20					25					30
205	Gly	Phe	Phe	Leu	Leu	Gly	Phe	Leu	Phe	Gly	Trp	Phe	Ile	Lys	Ser
206					35					40					45
207	Ser	Asn	Glu	Ala	Thr	Asn	Ile	Thr	Pro	Lys	His	Asn	Met	Lys	Ala
208					50					55					60
209	Phe	Leu	Asp	Glu	Leu	Lys	Ala	Glu	Asn	Ile	Lys	Lys	Phe	Leu	Tyr
210					65					70					75
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213	Gln	Leu	Ala	Lys	Gln	Ile	Gln	Ser	Gln	Trp	Lys	Glu	Phe	Gly	Leu
214					95					100					105
215	Asp	Ser	Val	Glu	Leu	Ala	His	Tyr	Asp	Val	Leu	Leu	Ser	Tyr	Pro
216					110					115					120
217	Asn	Lys	Thr	His	Pro	Asn	Tyr	Ile	Ser	Ile	Ile	Asn	Glu	Asp	Gly
218					125					130					135
219	Asn	Glu	Ile	Phe	Asn	Thr	Ser	Leu	Phe	Glu	Pro	Pro	Pro	Pro	Gly
220					140					145					150
221	Tyr	Glu	Asn	Val	Ser	Asp	Ile	Val	Pro	Pro	Phe	Ser	Ala	Phe	Ser
222					155					160					165
223	Pro	Gln	Gly	Met	Pro	Glu	Gly	Asp	Leu	Val	Tyr	Val	Asn	Tyr	Ala
224					170					175					180
225	Arg	Thr	Glu	Asp	Phe	Phe	Lys	Leu	Glu	Arg	Asp	Met	Lys	Ile	Asn
226					185					190					195
227	Cys	Ser	Gly	Lys	Ile	Val	Ile	Ala	Arg	Tyr	Gly	Lys	Val	Phe	Arg
228					200					205					210
229	Gly	Asn	Lys	Val	Lys	Asn	Ala	Gln	Leu	Ala	Gly	Ala	Lys	Gly	Val
230					215					220					225
231	Ile	Leu	Tyr	Ser	Asp	Pro	Ala	Asp	Tyr	Phe	Ala	Pro	Gly	Val	Lys
232					230					235					240
233	Ser	Tyr	Pro	Asp	Gly	Trp	Asn	Leu	Pro	Gly	Gly	Gly	Val	Gln	Arg
234					245					250					255
235	Gly	Asn	Ile	Leu	Asn	Leu	Asn	Gly	Ala	Gly	Asp	Pro	Leu	Thr	Pro
236					260					265					270
237	Gly	Tyr	Pro	Ala	Asn	Glu	Tyr	Ala	Tyr	Arg	Arg	Gly	Ile	Ala	Glu
238					275					280					285
239	Ala	Val	Gly	Leu	Pro	Ser	Ile	Pro	Val	His	Pro	Ile	Gly	Tyr	Tyr
240					290					295					300
241	Asp	Ala	Gln	Lys	Leu	Leu	Glu	Lys	Met	Gly	Gly	Ser	Ala	Pro	Pro
242					305					310					315
243	Asp	Ser	Ser	Trp	Arg	Gly	Ser	Leu	Lys	Val	Pro	Tyr	Asn	Val	Gly

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L:138 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:3